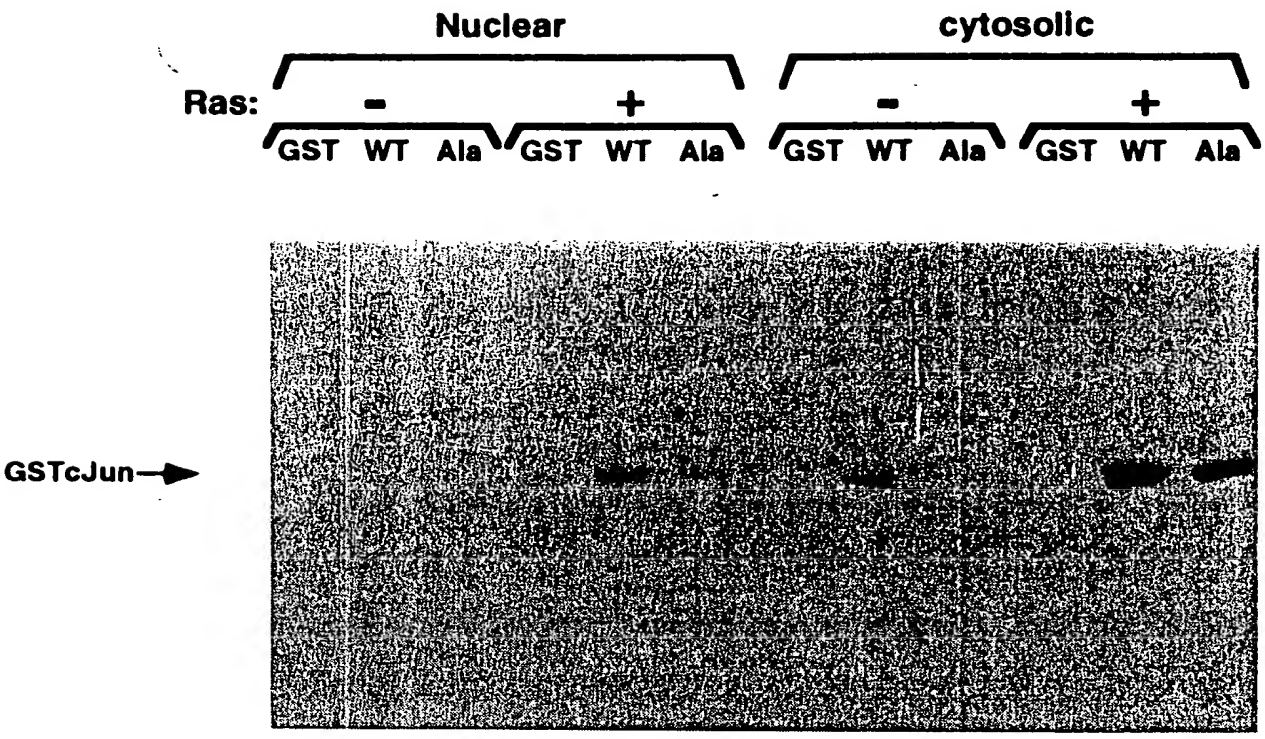

Nuclear
cytosolic
Ras:
-
+
-
+
GST WT Ala
GST WT Ala
GST WT Ala
GST WT Ala
GSTcJun

FIG. 1

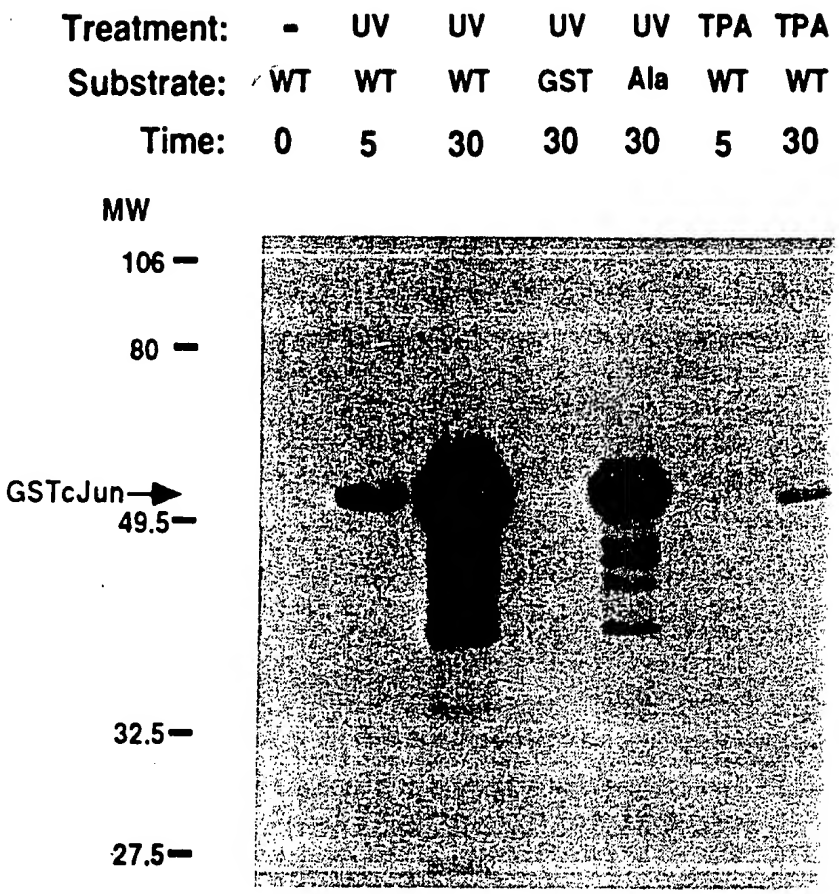


FIG. 2A

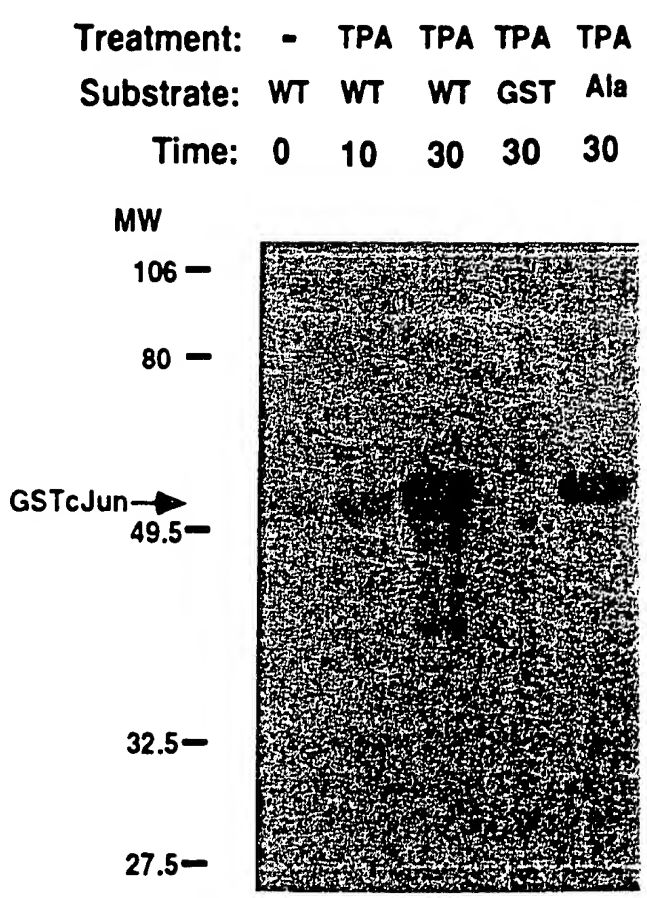


FIG. 2B

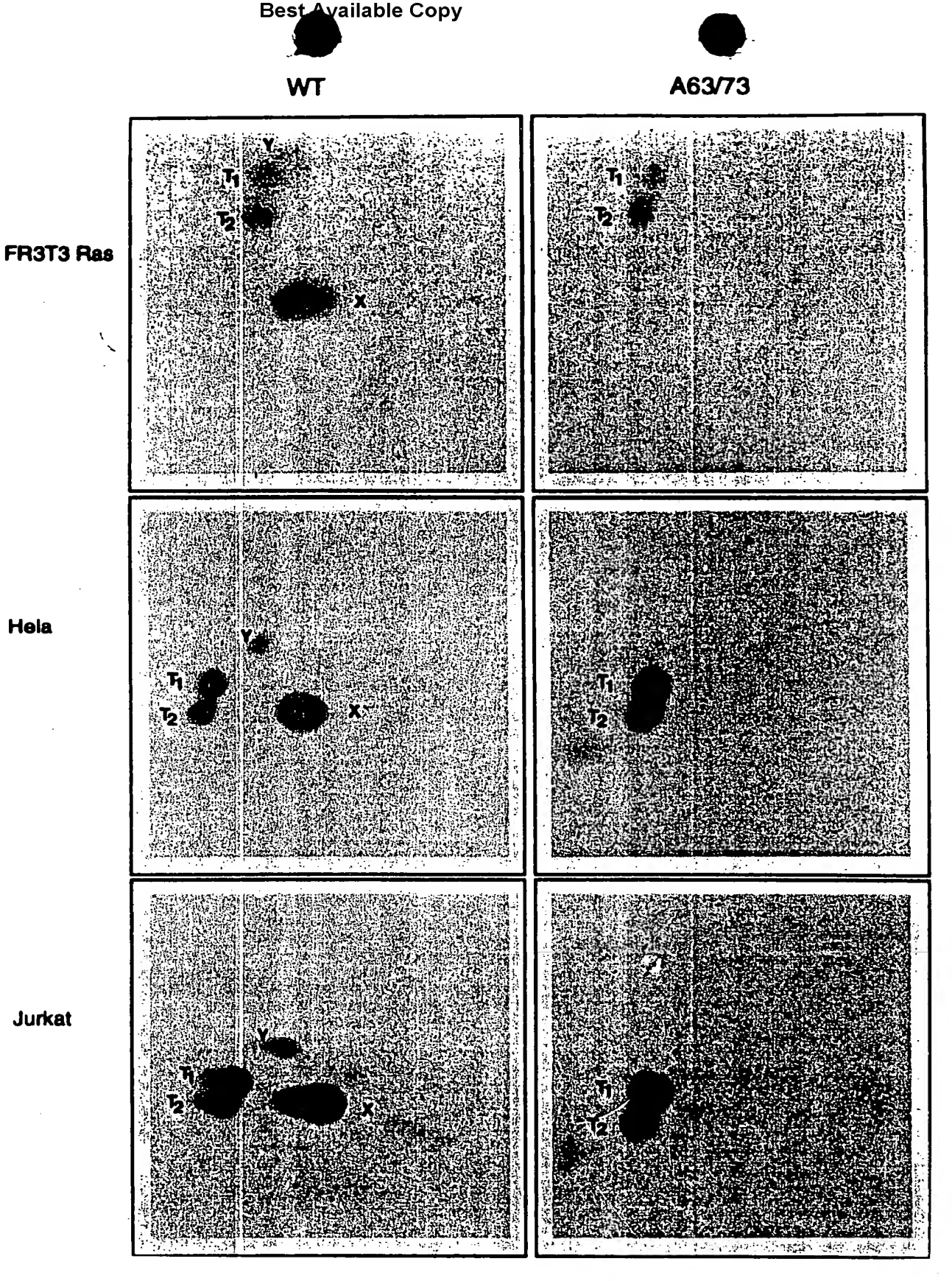


FIG. 3A

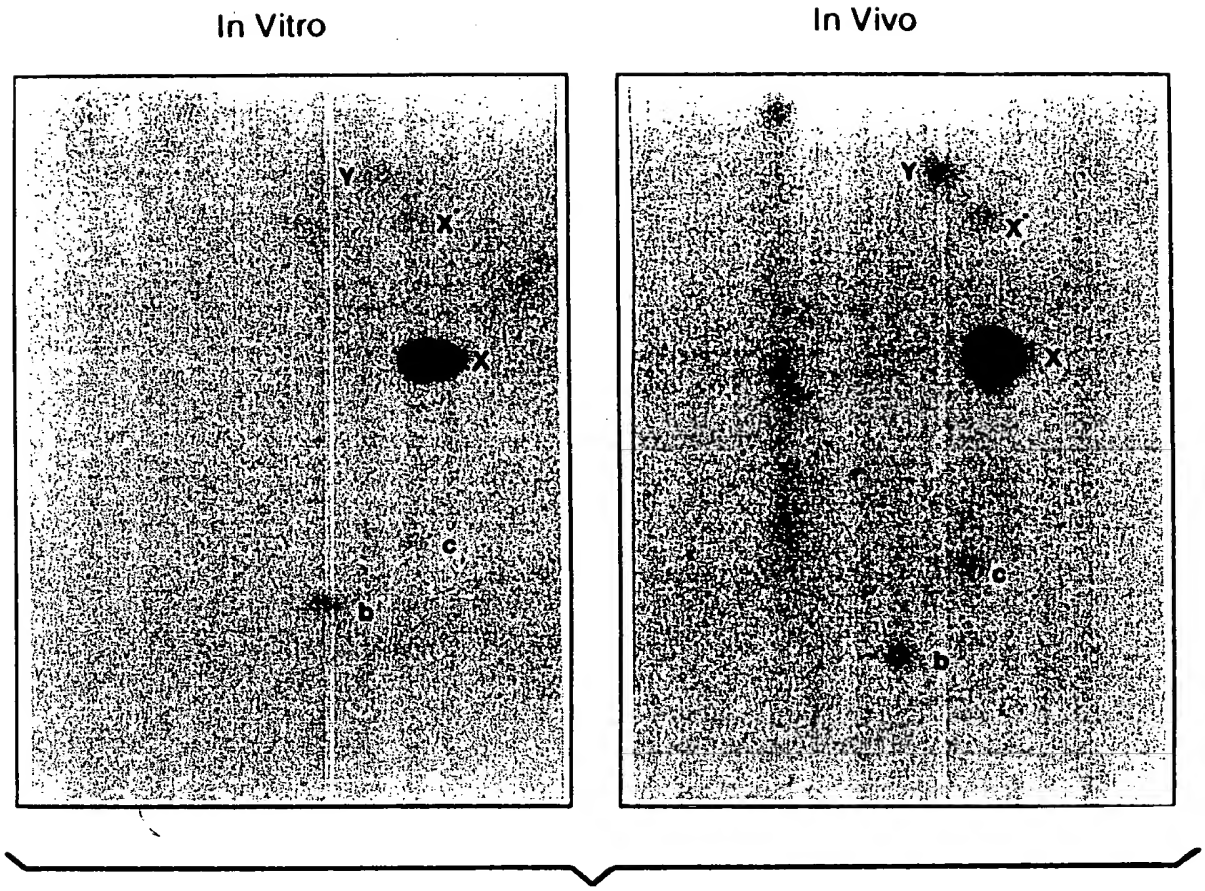


FIG. 3B

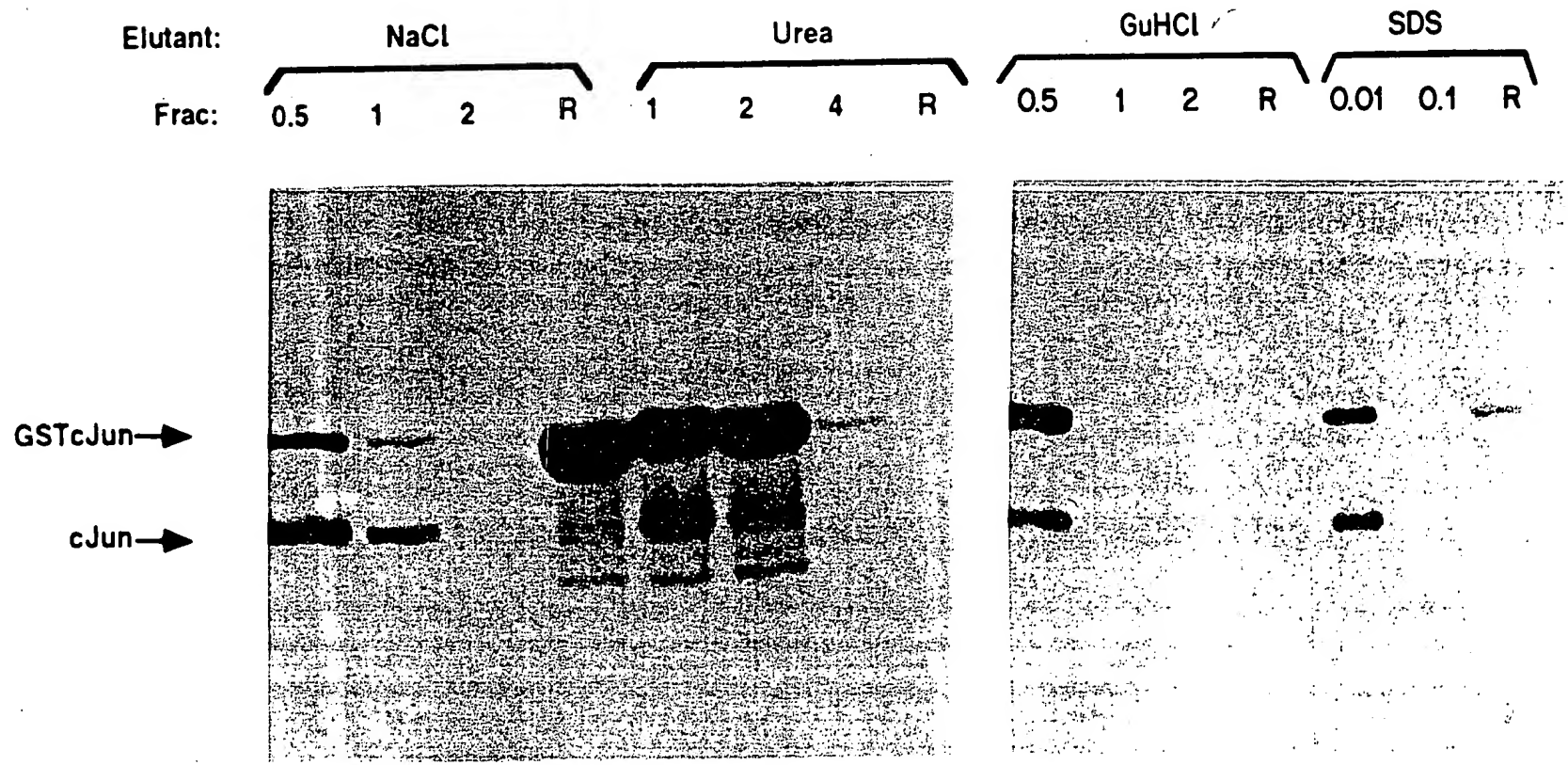


FIG. 4A

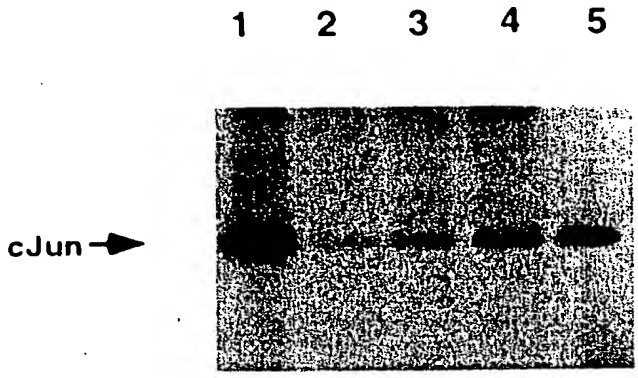


FIG. 4B

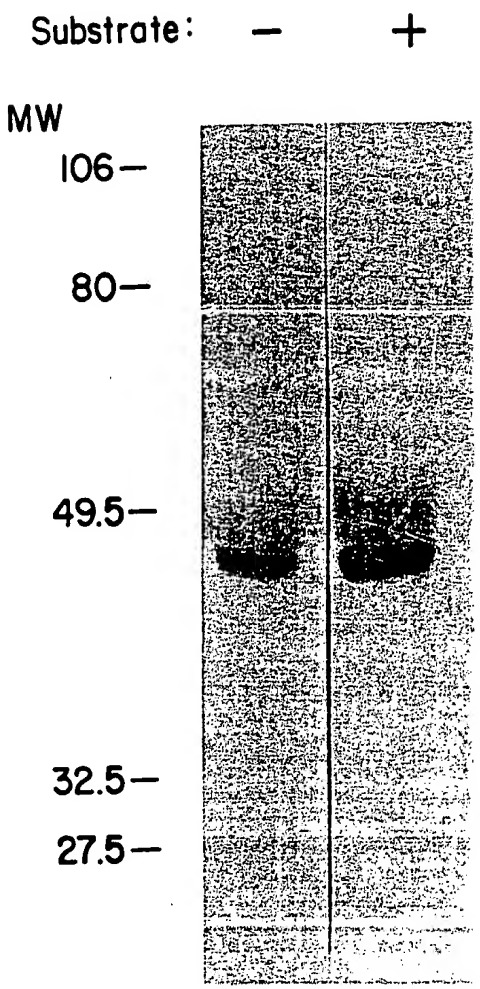

Substrate: – +
MW
106–
80–
49.5–
32.5–
27.5–

FIG. 5A

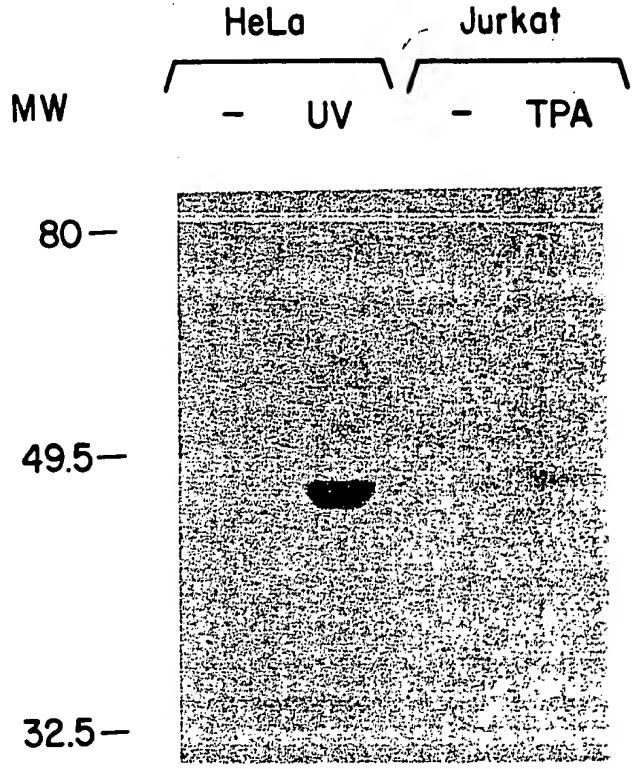

HeLa
Jurkat
MW
– UV
– TPA
80–
49.5–
32.5–

FIG. 5B

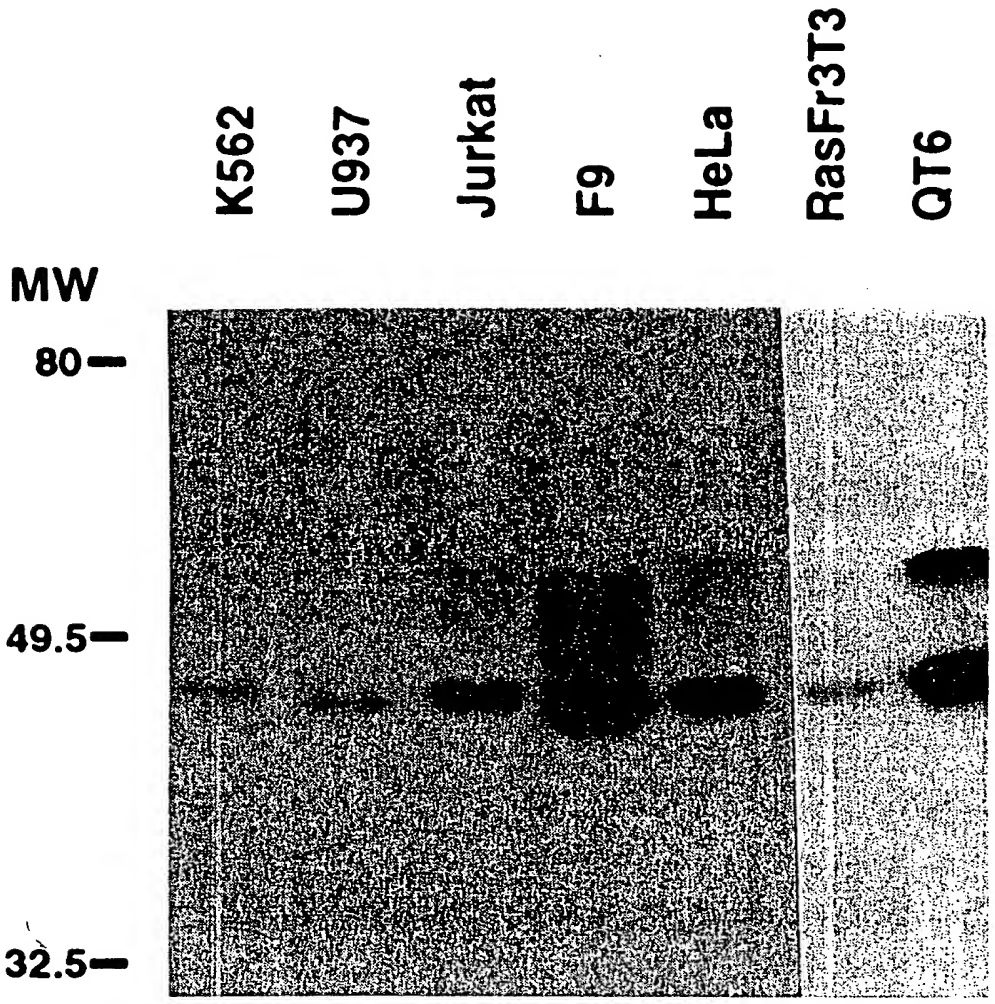


FIG. 5C

GST
GSTcJ(1-223)
GSTcJ(11-223)
GSTcJ(22-223)
GSTcJ(33-223)
GSTcJ(43-223)
GSTcJ(56-223)
GSTcJ(1-93)
GSTcJ(1-79)

Protein Gel

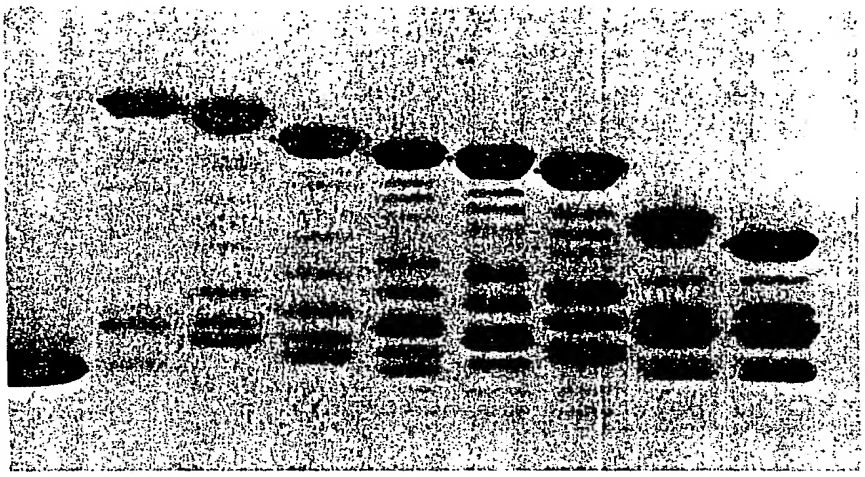


FIG.6A

^{32}P-Immobilized Substrate

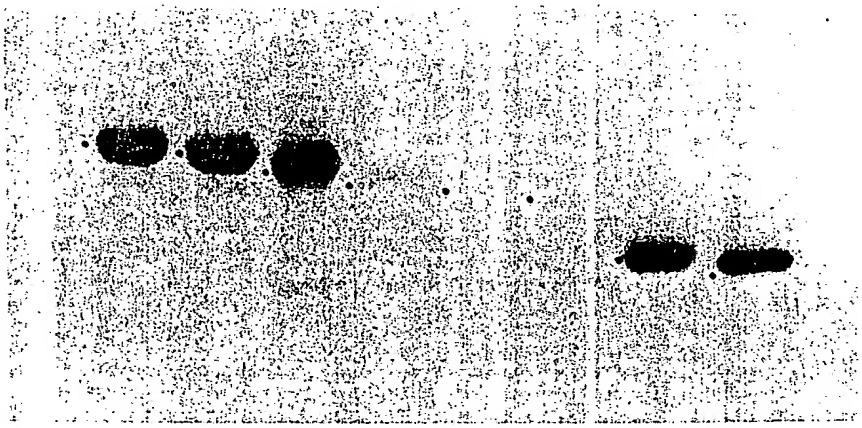


FIG.6B

^{32}P-Exogenous Substrate

GST
GSTcJ(1-223)
GSTcJ(11-223)
GSTcJ(22-223)
GSTcJ(33-223)
GSTcJ(43-223)
GSTcJ(56-223)
GSTcJ(1-93)
GSTcJ(1-79)

FIG.6C

FIG. 7A

FIG. 7B

FIG. 7C

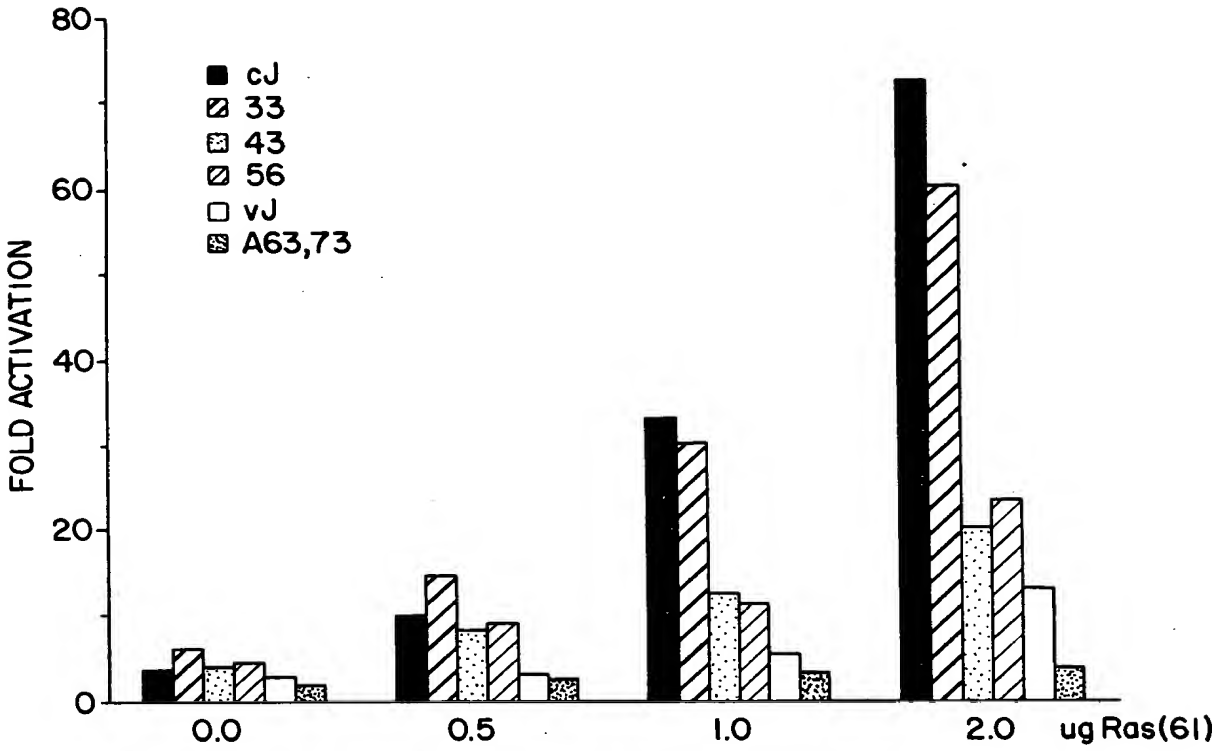

80
60
40
20
0
FOLD ACTIVATION
cJ
33
43
56
vJ
A63,73
0.0
0.5
1.0
2.0
ug Ras(61)

FIG. 8A

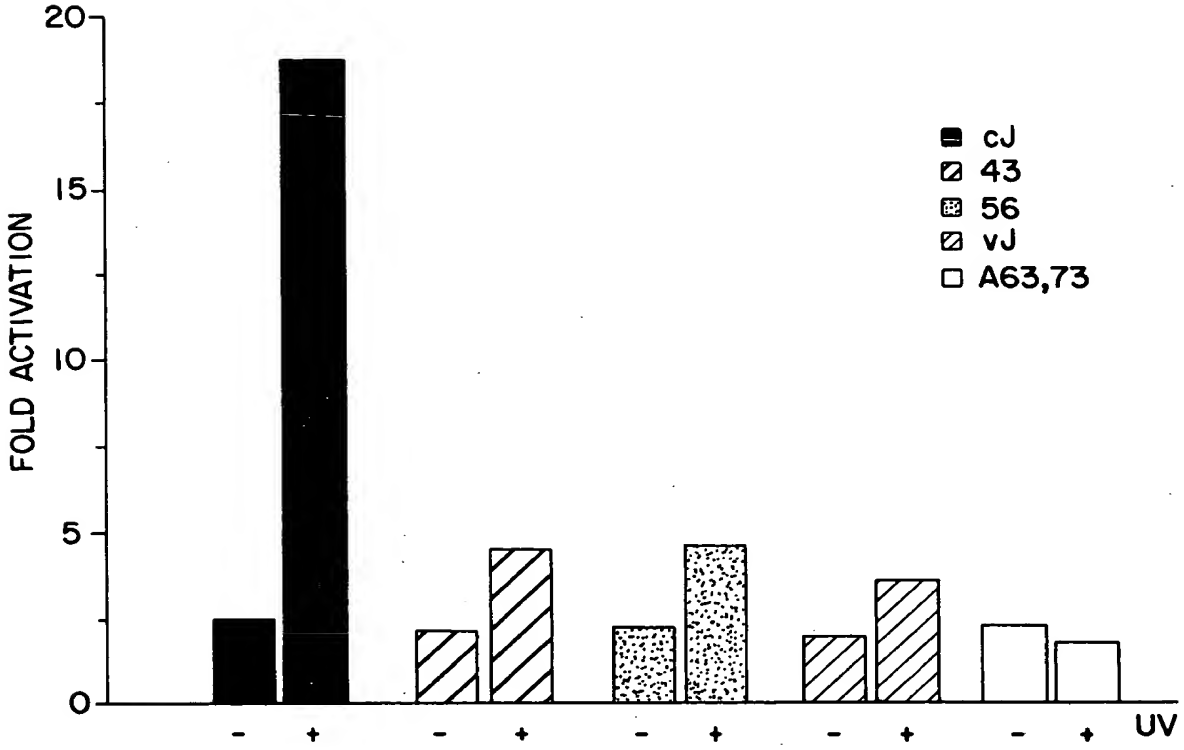

20
15
10
5
0
FOLD ACTIVATION
cJ
43
56
vJ
A63,73
- + - + - + - + - +
UV

FIG 8B

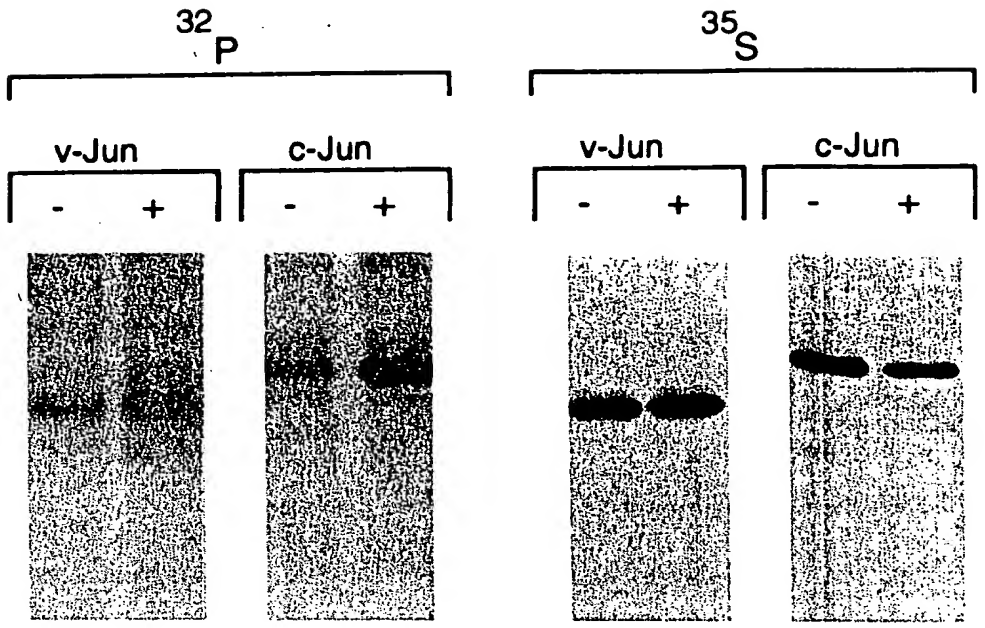


FIG. 9A

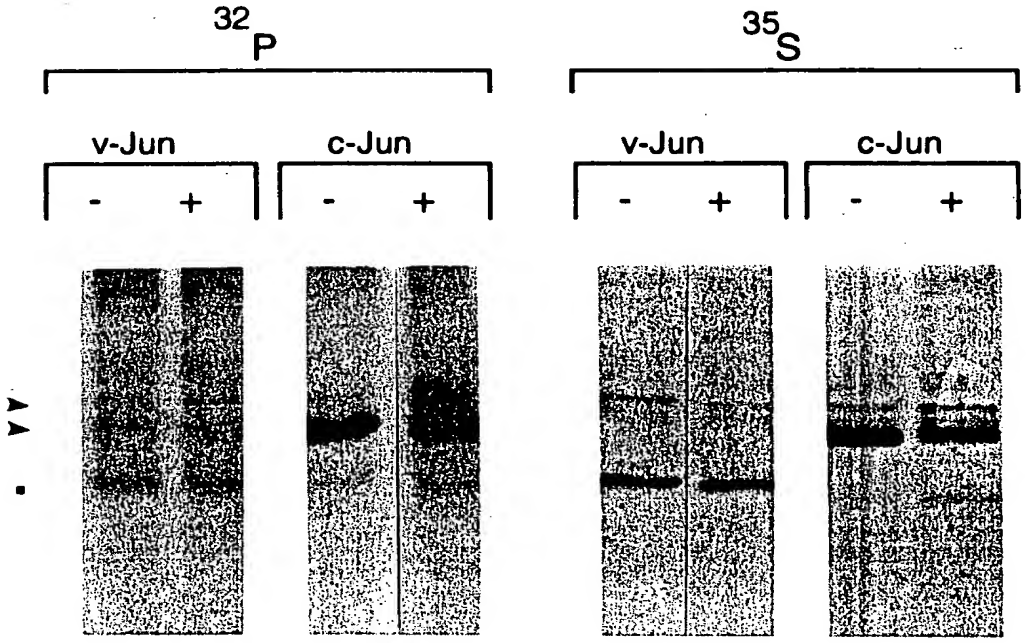


FIG. 9B

```
GAATTCCGGG GCGGCCAAGA CCCGCCGCCG GCCGGCCACT GCAGGGTCCG CACTGATCCG      60

CTCCGGCGGA GAGCCGCTGC TCTGGGAAGT CAGTTCGCCT GCGGACTCCG AGGAACCGCT     120

GCGCACGAAG AGCCGTCAGT GAGTGACCGC GACTTTTCAA AGCCGGGTAG GGCGCGCGAG     180

TCGACAAGTA AGAGTGCGGG AGGCATCTTA ATTAACCCTG CGCTCCCTGG AGCAGCTGGT     240

GAGGAGGGCG CACGGGGACG ACAGCCAGCG GGTGCGTGCG CTCTTAGAGA AACTTTCCCT     300

GTCAAAGGCT CCGGGGGGCG CGGGTGTCCC CCGCTTGCCA CAGCCCTGTT GCGGCCCCGA     360

AACTTGTGCG CGCACGCCAA ACTAACCTCA CGTGAAGTGA CGGACTGTTC T ATG ACT      417
                                                          Met Thr
                                                            1

GCA AAG ATG GAA ACG ACC TTC TAT GAC GAT GCC CTC AAC GCC TCG TTC        465
Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala Ser Phe
          5                  10                  15

CTC CCC TCC GAG AGG GGA CCT TAT GGC TAC AGT AAC CCC AAG ATC CTG        513
Leu Pro Ser Glu Arg Gly Pro Tyr Gly Tyr Ser Asn Pro Lys Ile Leu
     20                  25                  30

AAA CAG AGC ATG ACC CTG AAC CTG GCC GAC CCA GTG GGG AGC CTG AAG        561
Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser Leu Lys
 35                  40                  45                  50
```

FIG.10A

```
CCG CAC CTC CGC GCC AAG AAC TCG GAC CTC CTC ACC TCG CCC GAC GTG          609
Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro Asp Val
                    55                  60                  65

GGG CTG CTC AAG CTG GCG TCG CCC GAG CTG GAG CGC CTG ATA ATC CAG          657
Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile Ile Gln
                70                  75                  80

TCC AGC AAC GGG CAC ATC ACC ACC ACG CCG ACC CCC ACC CAG TTC CTG          705
Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln Phe Leu
            85                  90                  95

TGC CCC AAG AAC GTG ACA GAT GAG CAG GAG GGG TTC GCC GAG GGC TTC          753
Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu Gly Phe
        100                 105                 110

GTG CGC GCC CTG GCC GAA CTG CAC AGC CAG AAC ACG CTG CCC AGC GTC          801
Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro Ser Val
    115                 120                 125                 130

ACG TCG GCG GCG CAG CCG GTC AAC GGG GCA GGC ATG GTG GCT CCC GCG          849
Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala Pro Ala
                135                 140                 145

GTA GCC TCG GTG GCA GGG GGC AGC GGC AGC GGC GGC TTC AGC GCC AGC          897
Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser Ala Ser
            150                 155                 160
```

FIG. 10B

```
CTG CAC AGC GAG CCG CCG GTC TAC GCA AAC CTC AGC AAC TTC AAC CCA        945
Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe Asn Pro
        165                 170                 175

GGC GCG CTG AGC AGC GGC GGC GGG GCG CCC TCC TAC GGC GCG GCC GGC        993
Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala Ala Gly
    180                 185                 190

CTG GCC TTT CCC GCG CAA CCC CAG CAG CAG CAG CAG CCG CCG CAC CAC       1041
Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Gln Pro Pro His His
195                 200                 205                 210

CTG CCC CAG CAG ATG CCC GTG CAG CAC CCG CGG CTG CAG GCC CTG AAG       1089
Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala Leu Lys
                215                 220                 225

GAG GAG CCT CAG ATA GTG CCC GAG ATG CCC GGC GAG ACA CCG CCC CTG       1137
Glu Glu Pro Gln Ile Val Pro Glu Met Pro Gly Glu Thr Pro Pro Leu
            230                 235                 240

TCC CCC ATC GAC ATG GAG TCC CAG GAG CGC ATC AAG GCG GAG AGG AAG       1185
Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu Arg Lys
        245                 250                 255

CGC ATG AGG AAC CGC ATC GCT GCC TCG AAG TGC CGA AAA AGG AAG CTG       1233
Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg Lys Leu
    260                 265                 270
```

FIG. 10C

```
GAG AGA ATC GCC CGG CTG GAG GAA AAA GTG AAA ACC TTG AAA GCT CAG      1281
Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln
275                 280                 285                 290

AAC TCG GAG CTG GCG TCG ACG GCC AAC ATG CTC AGG GAA CAG GTC GCA      1329
Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala
                295                 300                 305

CAG CTT AAA CAC AAA GTC ATG AAC CAC GTT AAC AGT GGG TGC CAA CTC      1377
Gln Leu Lys His Lys Val Met Asn His Val Asn Ser Gly Cys Gln Leu
            310                 315                 320

ATC CTA ACG CAG CAG TTG CAA ACA TTT TGAAGAGAGA CCGTCGGGGG            1424
Ile Leu Thr Gln Gln Leu Gln Thr Phe
        325                 330

CTGAGGGGCA ACGAAGAAAA AAAATAACAC AGAGAGACAG ACTTGAGAAC TTGACAAGTT    1484

GCGACGGAGA GAAAAAAGAA GTGTCCGAGA ACTAAAGCCA AGGGTATCCA AGTTGGACTG    1544

GGTTCGGTCT GACGGCGCCC CCAGTGTGCA CGAGTGGGAA CCACCTGGTC GCGCCCTCCC    1604

TTGGCGTCGA GCCAGGGAGC GGCCGCCTGG GGGCTGCCCC GCTTTGCGGA CGGGCTGTCC    1664

CCGCGCGAAC GGAACGTTGG ACTTTCGTTA ACATTGACCA AGAACTGCAT GGACCTAACA    1724
```

FIG. 10D

```
TTCGATCTCA TTCAGTATTA AAGGGGGCAG GGGGAGGGGG TTACAAACTG CAATAGAGAC    1784
TGTAGATTGC TTCTGTAGTA CTCCTTAAGA ACACAAAGCG GGGGGAGGGT TGGGGAGGGG    1844
CGGCAGGAGG GAGGTTTGTG AGAGCGAGGC TGAGCCTACA GATGAACTCT TTCTGGCCTG    1904
CTTTCGTTAA CTGTGTATGT ACATATATAT ATTTTTTAAT TTGATTAAAG CTGATTACTG    1964
TCAATAAACA GCTTCATGCC TTTGTAAGTT ATTTCTTGTT TGTTTGTTTG GGATCCTGCC    2024
CAGTGTTGTT TGTAAATAAG AGATTTGGAG CACTCTGAGT TTACCATTTG TAATAAAGTA    2084
TATAATTTTT TT                                                        2096
```

FIG. 10E

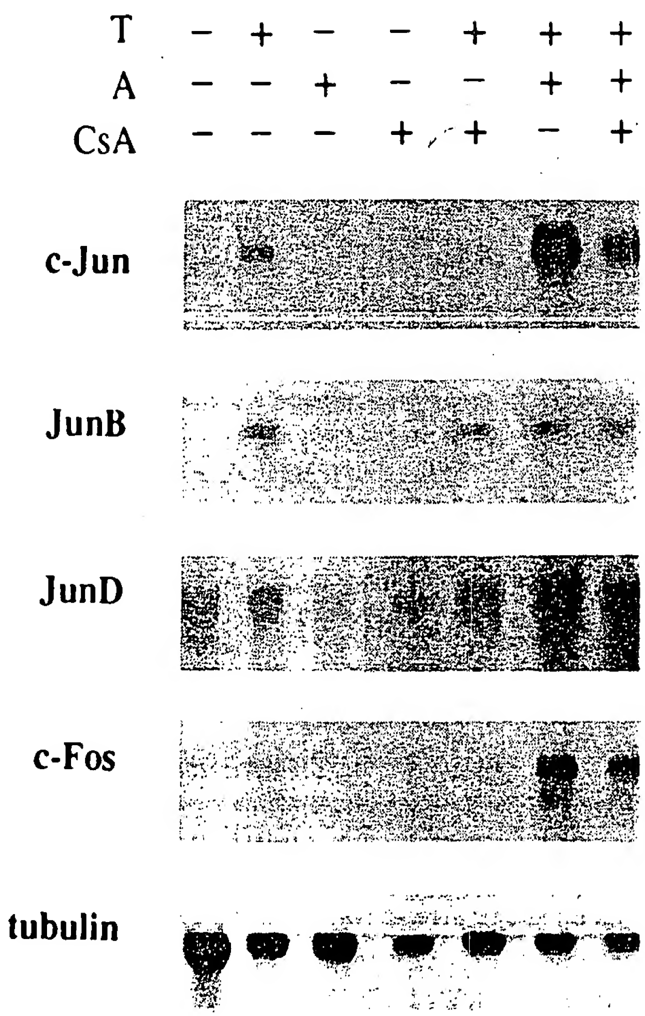


FIG.11A

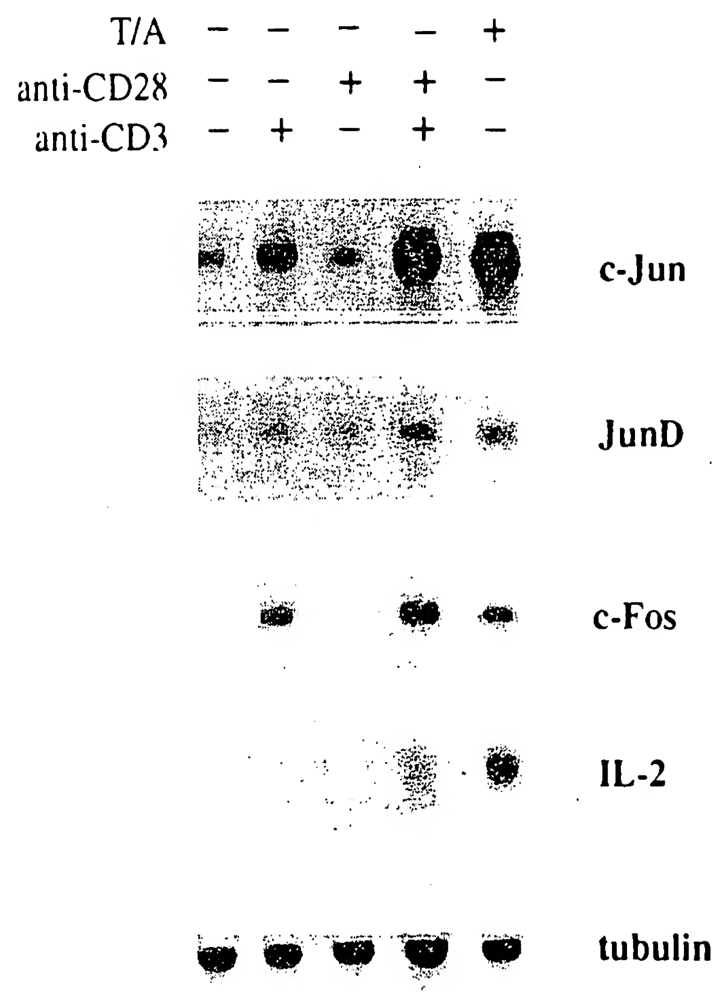


FIG.11B

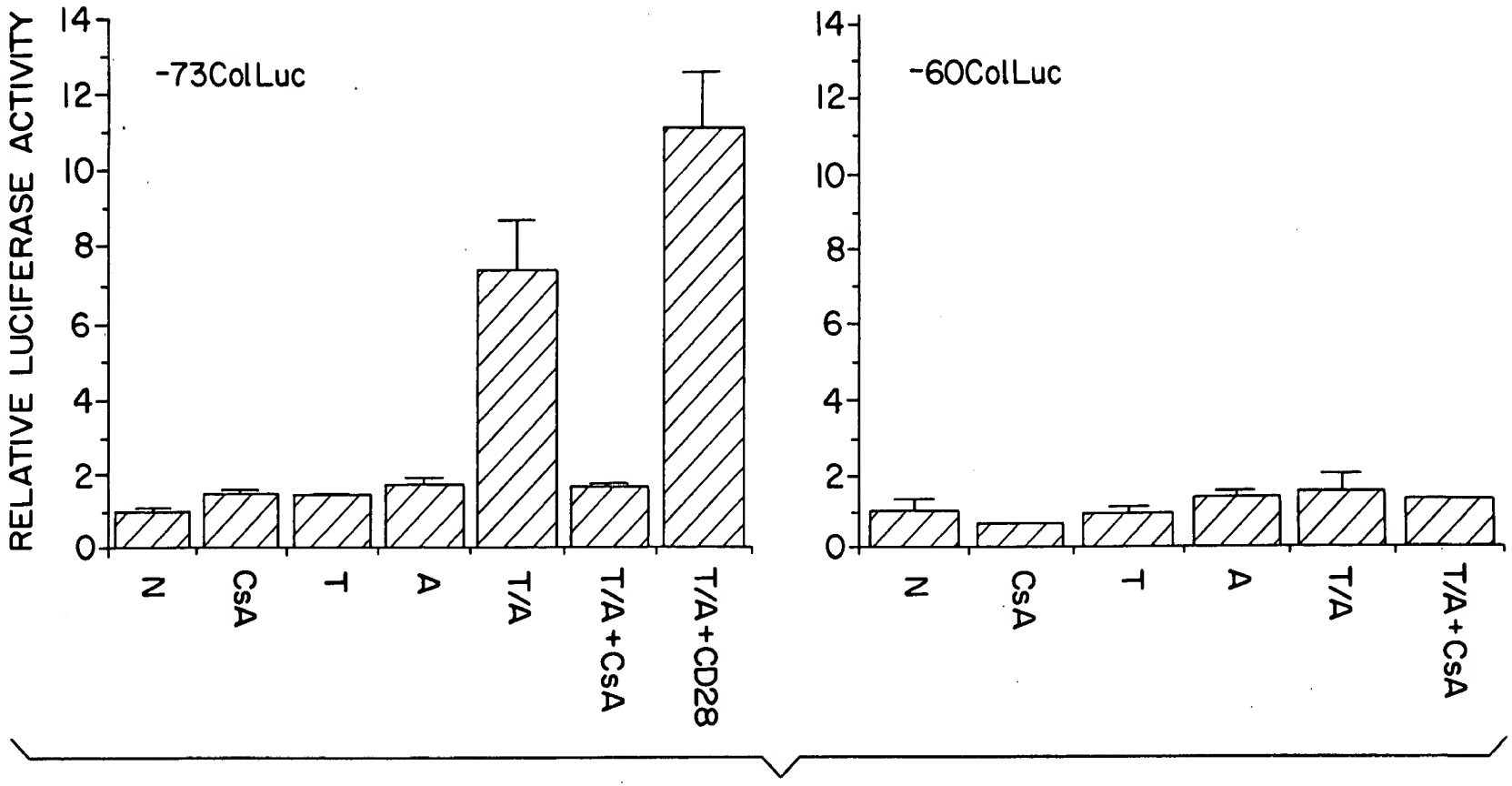

RELATIVE LUCIFERASE ACTIVITY
14
12
10
8
6
4
2
0
-73ColLuc
-60ColLuc
N
CsA
T
A
T/A
T/A+CsA
T/A+CD28

FIG. 11C

FIG. 12A

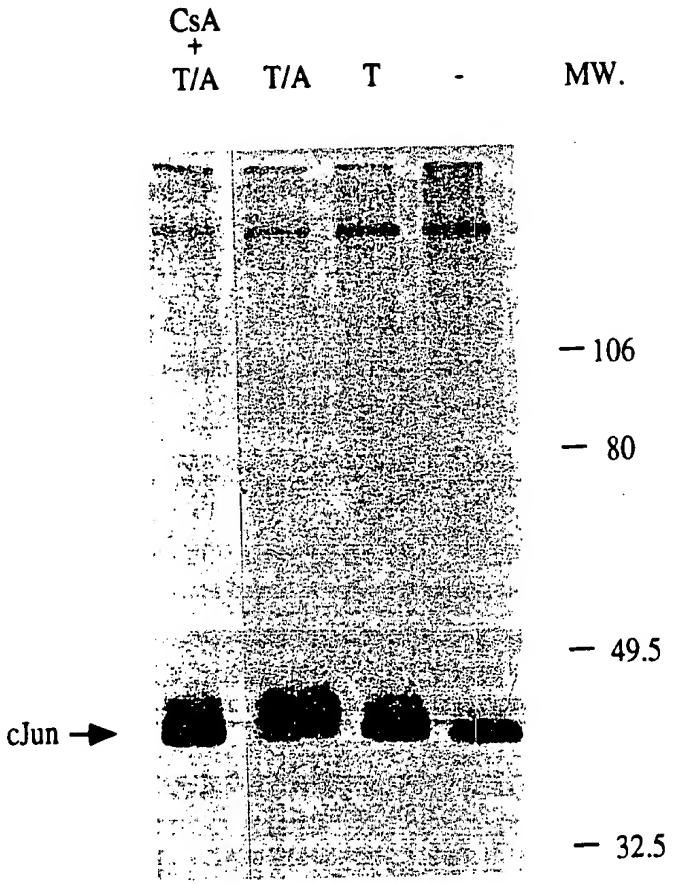
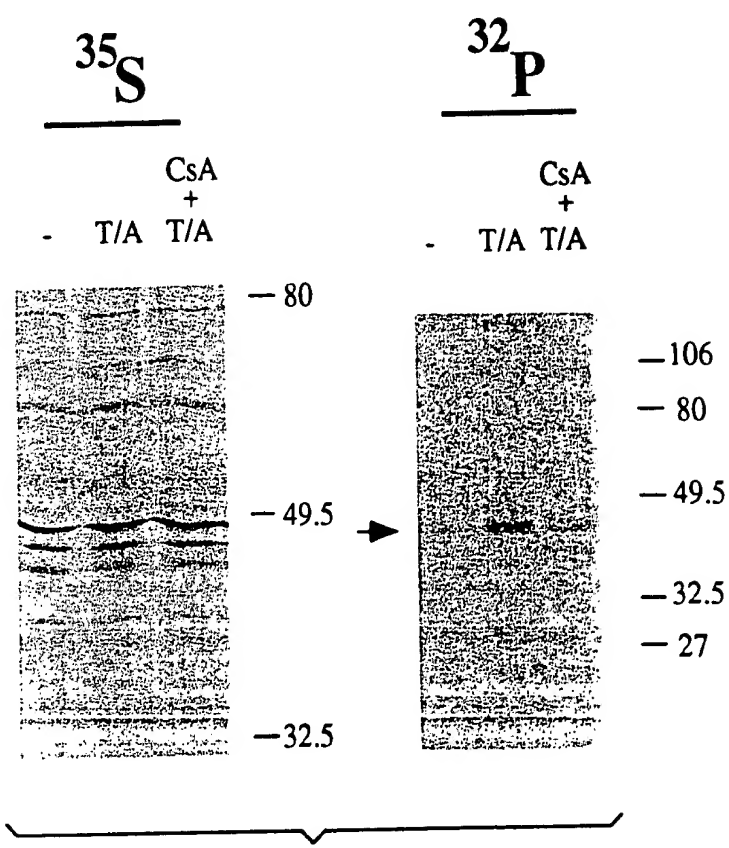


FIG. 12B



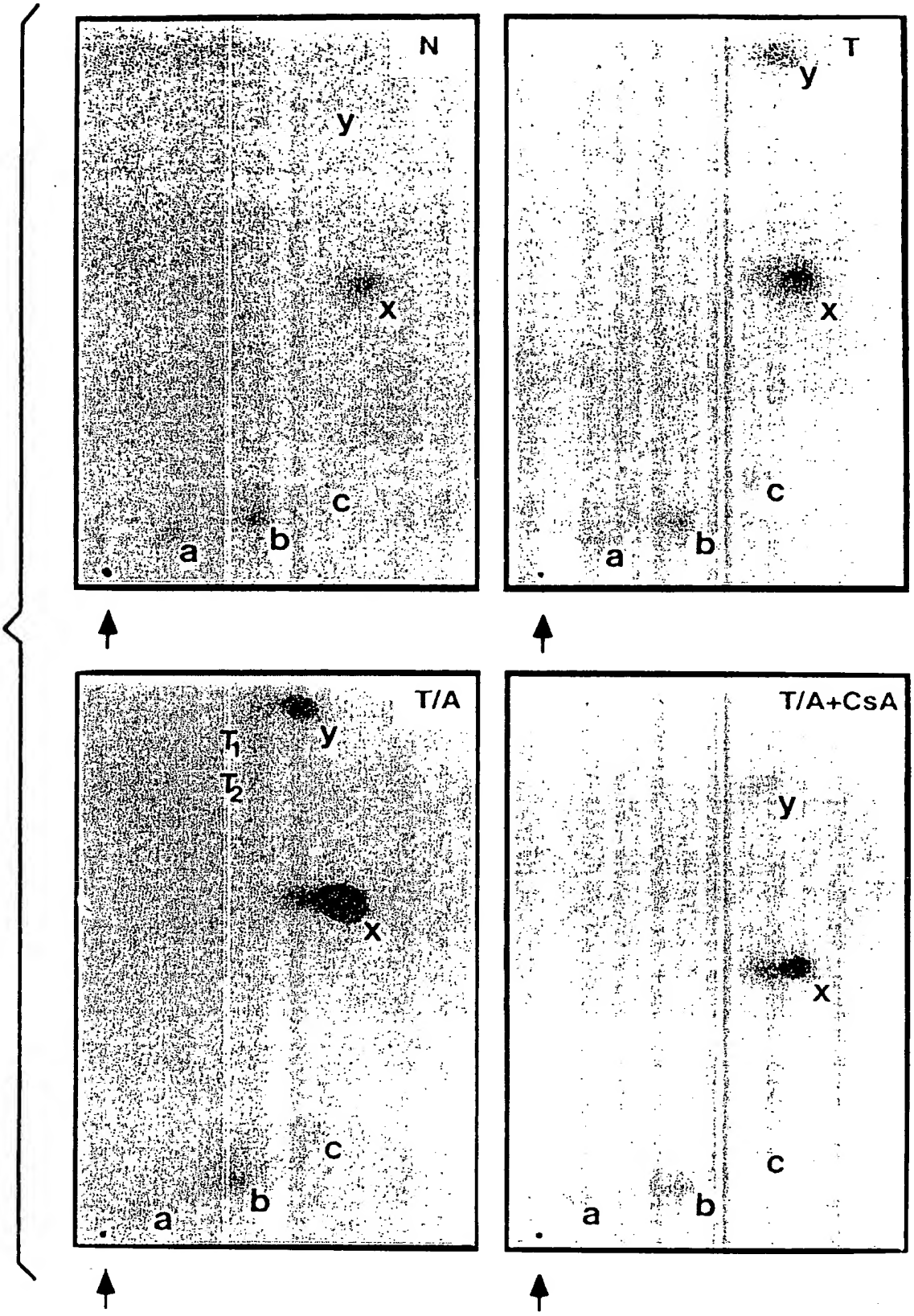


FIG.12C

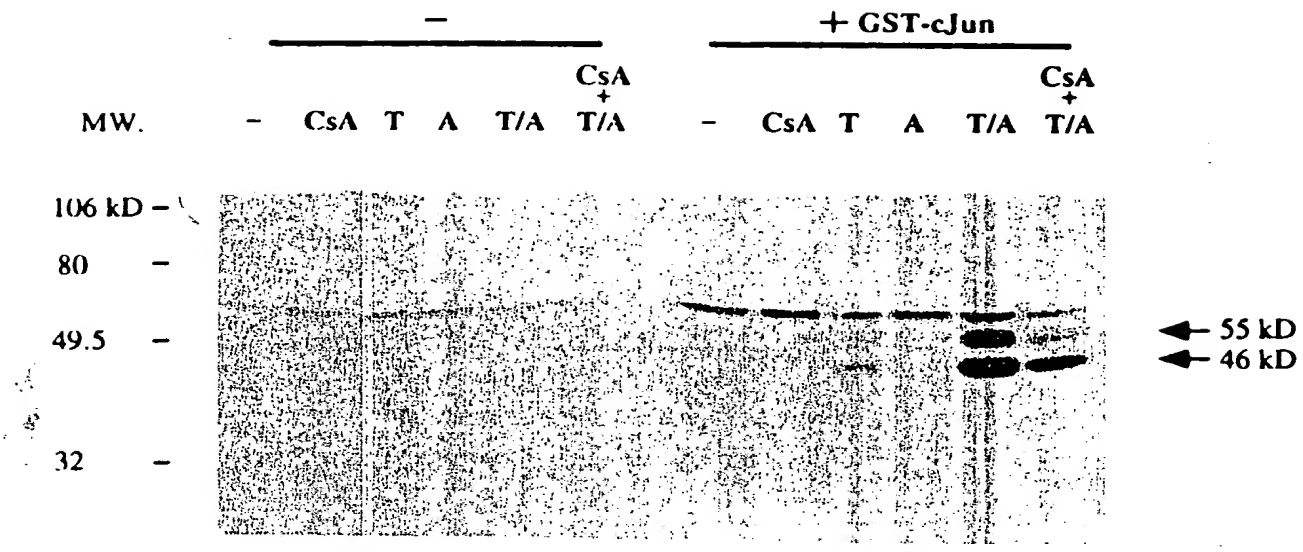


FIG.13A

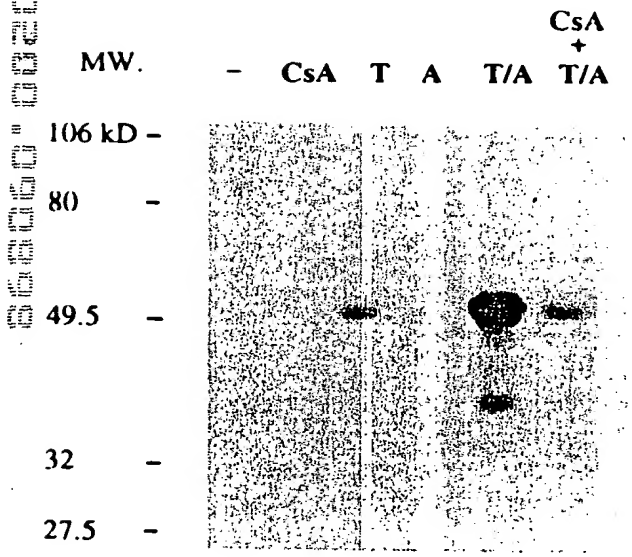


FIG.13B

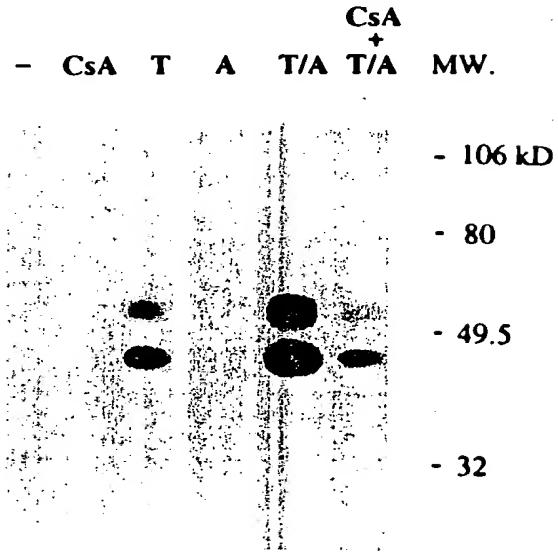


FIG.13C

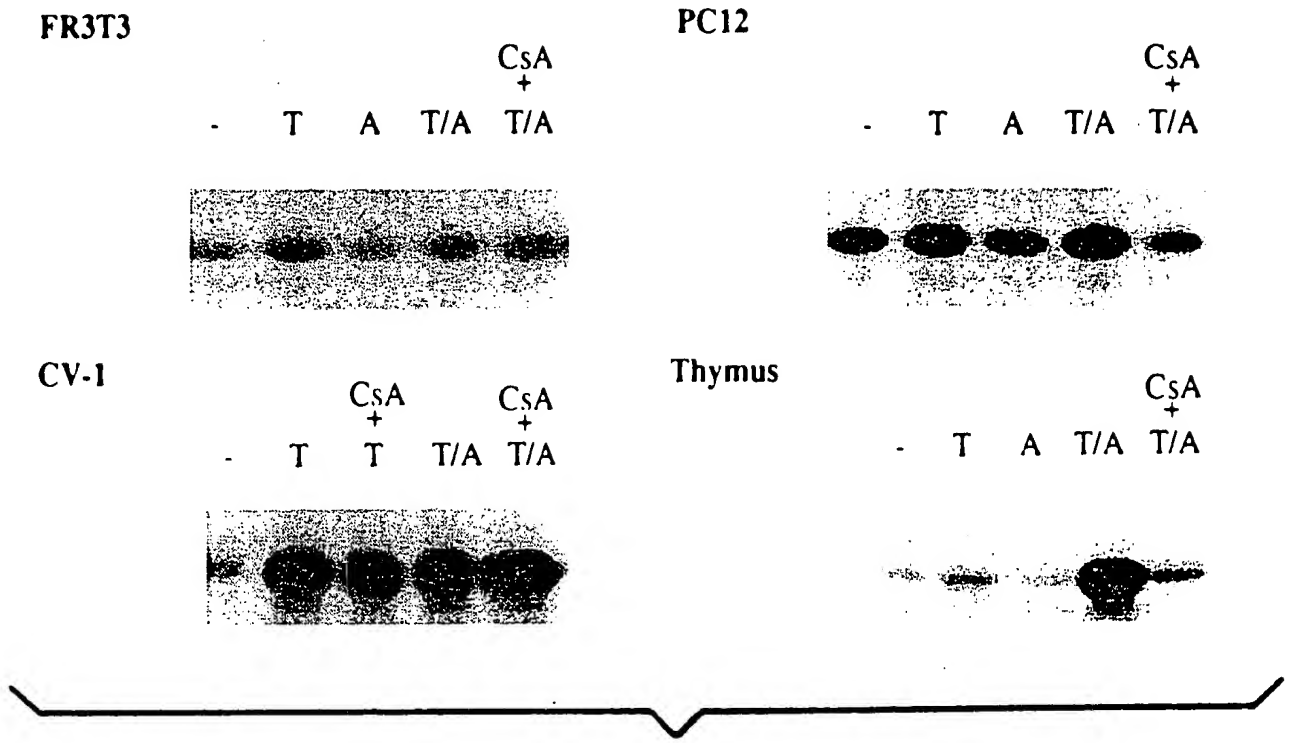


FIG.14

FIG.15A

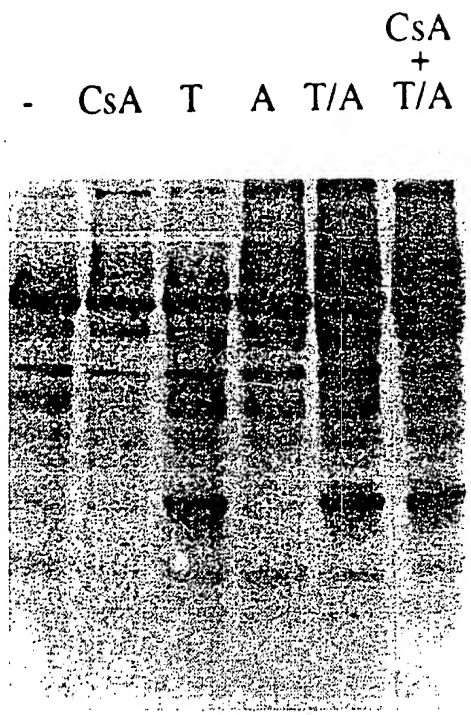


FIG.15B

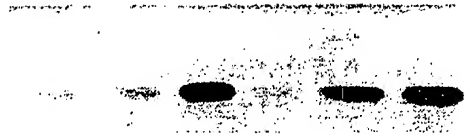


FIG.15C

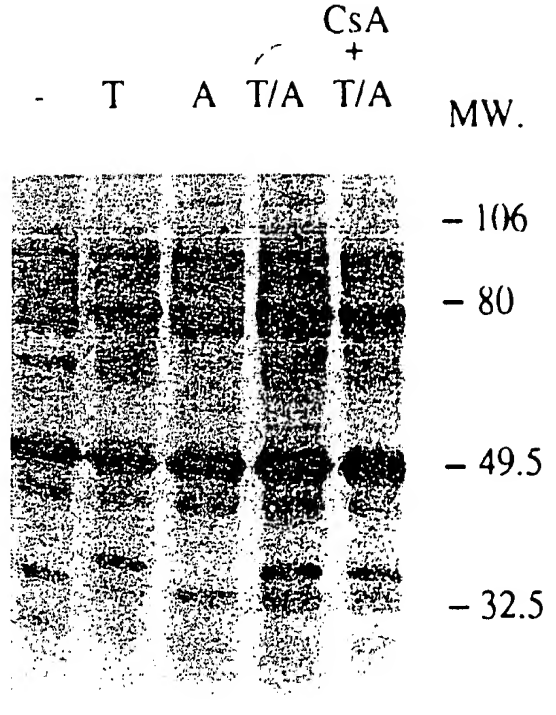


FIG.15D

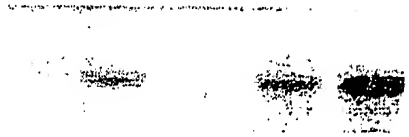


FIG. 16A

CsA	+	−	−	−	−
anti-CD28	+	+	−	+	−
anti-CD3	+	+	+	−	−

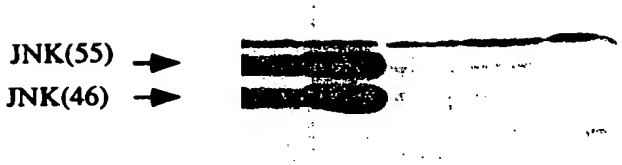


FIG. 16B

CsA	−	−	−	−	+
anti-CD28	−	−	+	+	+
anti-CD3	−	+	−	+	+

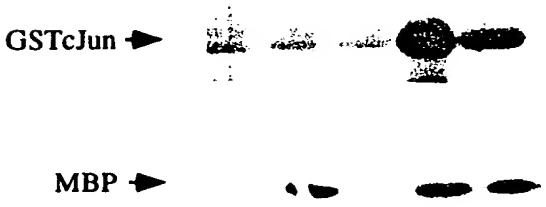
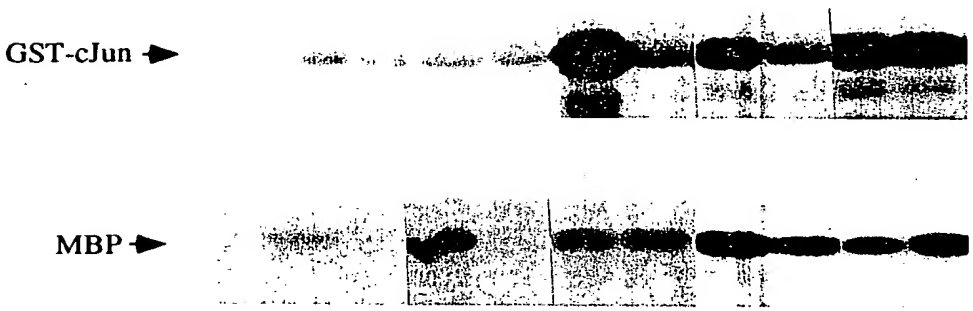


FIG. 16C

	1	2	3	4	5	6	7	8	9	10	11
CsA	−	−	−	−	−	−	+	−	+	−	+
anti-CD28	−	−	−	−	+	−	−	−	−	+	+
anti-CD3	−	−	−	+	−	−	−	+	+	−	−
A	−	−	+	−	−	+	+	−	−	−	−
T	−	+	−	−	−	+	+	+	+	+	+



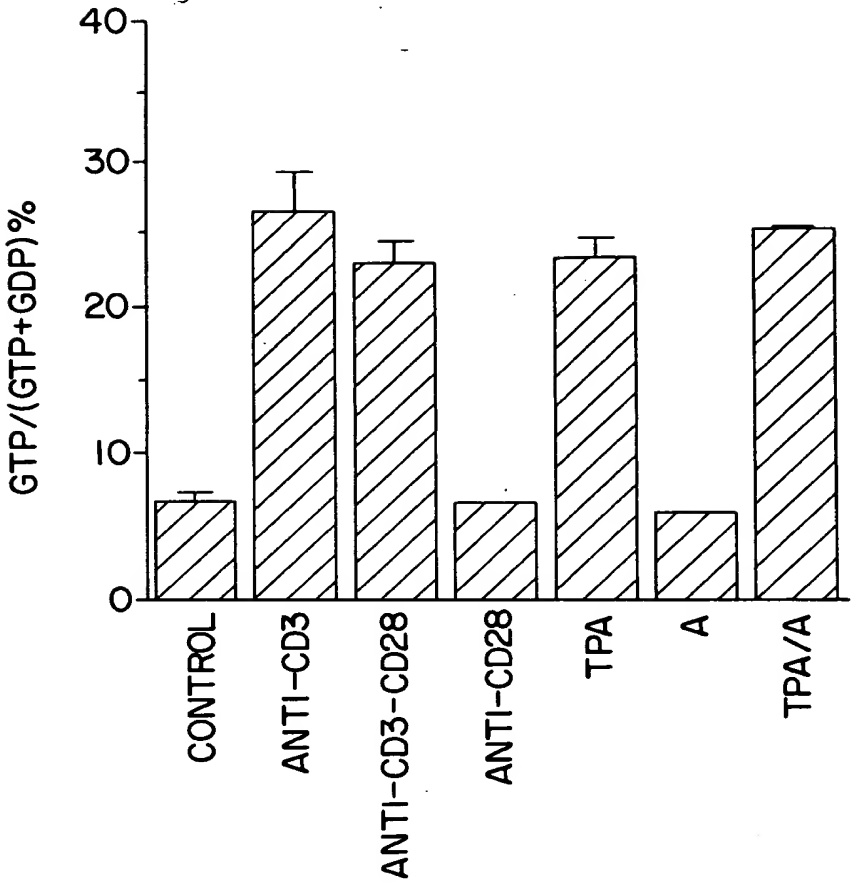


FIG. 17A

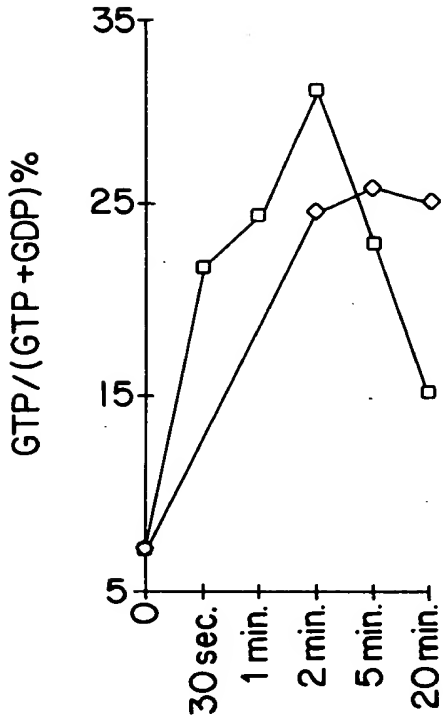


FIG. 17B